

(SEQ ID NO:14) (4), M978 (SEQ ID NO:15) (5), 1610 (SEQ ID NO:16) (6), 867 (SEQ ID NO:17) (7), S3032 (SEQ ID NO:18) (8), and 891 (SEQ ID NO:19) (9) Tbp2. The numbering of IM2169, as it appears in SEQ ID NO:2, is given in italics. The sequences which may be deleted according to a preferred embodiment appear in bold type. (C) indicates the consensus sequence.

Figures 5 to 7 illustrate the construction of the plasmids PTG5782, PTG5755 and PTG5783, respectively.

D1 Figure 10 presents the alignments to maximum homology of the sequences of the hinge domains (second domain) of IM2169 (SEQ ID NO: 11) (1), 2223 (SEQ ID NO:13) (2), 708 (SEQ ID NO:14) (3), M528 (SEQ ID NO:42) (4), 6940 (SEQ ID NO:12) (5), M978 (SEQ ID NO:15) (6), 1610 (SEQ ID NO:16) (7), S3032 (SEQ ID NO:18) (8), 867 (SEQ ID NO:17) (9), BZ83 (SEQ ID NO:40) (10) and BZ163 (SEQ ID NO:41) (11) Tbp2. The numbering of IM2169, as it appears in SEQ ID NO:2, is given in italics. The sequences which may be deleted according to a preferred embodiment appear in bold type. (C) indicates the consensus sequence.--

IN THE CLAIMS:

Please amend the claims as follows:

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D1
2 --54. (Once amended) A polypeptide having an amino acid sequence which is [derived] obtained from the sequence of the Tbp2 subunit of the transferrin receptor of a [Neisseria meningitidis] Neisseria meningitidis strain of type IM2169 or IM2394, whose first, second and third domains are defined by [maximal homology